

SEQUENCE LISTING

<110> Issa, Jean-Pierre

<120> CACNA1G POLYNUCLEOTIDE POLYPEPTIDE AND
METHODS OF USE THEREFOR

<130> JHU1590

<140> 09/398,522

<141> 1999-09-15

<160> 120

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CACNA1G

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<210> 39
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<212> DNA

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<212> DNA

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<223> CACNA1G - a gene encoding a T-type calcium channel

<221> CDS

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cgtgaggaca cctcctctga gggcgccgc ttgccctct cgggatcgcc cggggccccc 360
gctggccaga gg atg gac gag gag gat gga ggc ggc gcc gag gag tgc 411
Met Asp Glu Glu Glu Asp Gly Ala Gly Ala Glu Glu Ser

1

5

10

13

gga cag ccc cgg agc ttc atg cgg ctc aac gac ctg tgc ggg gcc ggg Gly Gln Pro Arg Ser Phe Met Arg Leu Asn Asp Leu Ser Gly Ala Gly 15 20 25	459
ggc cgg ccg ggg ccg ggg tca gca gaa aag gac ccg ggc agc gcc gac Gly Arg Pro Gly Pro Gly Ser Ala Glu Lys Asp Pro Gly Ser Ala Asp 30 35 40 45	507
tcc gag gcc gag ggg ctg ccg tac ccg gcc ctg gcc ccg gtg gtt ttc Ser Glu Ala Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe 50 55 60	555
ttc tac ttg agc cag gac agc cgc ccg cgg agc tgg tgt ctc cgc acg Phe Tyr Leu Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr 65 70 75	603
gtc tgt aac ccc tgg ttt gag cgc atc agc atg ttg gtc atc ctt ctc Val Cys Asn Pro Trp Phe Glu Arg Ile Ser Met Leu Val Ile Leu Leu 80 85 90	651
aac tgc gtg acc ctg ggc atg ttc cgg cca tgc gag gac atc gcc tgt Asn Cys Val Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys 95 100 105	699
gac tcc cag cgc tgc cgg atc ctg cag gcc ttt gat gac ttc atc ttt Asp Ser Gln Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe 110 115 120 125	747
gcc ttc ttt gcc gtg gag atg gtg gtg aag atg gtg gcc ttg ggc atc Ala Phe Phe Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile 130 135 140	795
ttt ggg aaa aag tgt tac ctg gga gac act tgg aac cgg ctt gac ttt Phe Gly Lys Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe 145 150 155	843
ttc atc gtc atc gca ggg atg ctg gag tac tgc ctg gac ctg cag aac Phe Ile Val Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn 160 165 170	891
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gcc att aac cgg gtg ccc agc atg cgc atc ctt gtc acg ttg ctg ctg Ala Ile Asn Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu 190 195 200 205	987
gat acg ctg ccc atg ctg ggc aac gtc ctg ctg ctc tgc ttc ttc gtc Asp Thr Leu Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val 210 215 220	1035
ttc ttc atc ttc ggc atc gtc ggc gtc cag ctg tgg gca ggg ctg ctt Phe Phe Ile Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu 225 230 235	1083
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14

gac ctg gag cgc tat tac cag aca gag aac gag gat gag agc ccc ttc Asp Leu Glu Arg Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe 255 260 265	1179
atc tgc tcc cag cca cgc gag aac ggc atg cgg tcc tgc aga agc gtg Ile Cys Ser Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val 270 275 280 285	1227
ccc acg ctg cgc ggg gac ggg ggc ggt ggc cca cct tgc ggt ctg gac Pro Thr Leu Arg Gly Asp Gly Gly Gly Gly Pro Pro Cys Gly Leu Asp 290 295 300	1275
tat gag gcc tac aac agc tcc agc aac acc acc tgt gtc aac tgg aac Tyr Glu Ala Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn 305 310 315	1323
cag tac tac acc aac tgc tca gcg ggg gag cac aac ccc ttc aag ggc Gln Tyr Tyr Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly 320 325 330	1371
gcc atc aac ttt gac aac att ggc tat gcc tgg atc gcc atc ttc cag Ala Ile Asn Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln 335 340 345	1419
gtc atc acg ctg gag ggc tgg gtc gac atc atg tac ttt gtg atg gat Val Ile Thr Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp 350 355 360 365	1467
gct cat tcc ttc tac aat ttc atc tao ttc acc ctc ctc atc atc gtg Ala His Ser Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val 370 375 380	1515
ggc tcc ttc ttc atg atc aac ctg tgc ctg ggc gtg att gcc acg cag Gly Ser Phe Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln 385 390 395	1563
ttc tca gag acc aag cag cgg gaa agc cag ctg atg cgg gag cag cgt Phe Ser Glu Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg 400 405 410	1611
gtg cgg ttc ctg tcc aac gcc agc acc ctg gct agc ttc tct gag ccc Val Arg Phe Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Pro 415 420 425	1659
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ccc agc agc agc tgc tct cgc tcc cac cgc cgc cta tcc gtc cac cac Pro Ser Ser Ser Cys Ser Arg Ser His Arg Arg Leu Ser Val His His 480 485 490	1851

15

ctg gtg cac cac cac cac cat cac cac cac tac cac ctg ggc aat Leu Val His His His His His His His His His Tyr His Leu Gly Asn 495 500 505	1899
ggg aag ctc agg gcc ccc egg gcc agc cgg gag atc cag gac agg gat Gly Thr Leu Arg Ala Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp 510 515 520 525	1947
gcc aat ggg tcc cgc egg ctc atg ctg cca cca ccc tgg acg cct gcc Ala Asn Gly Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Ala 530 535 540	1995
ctc tcc ggg gcc ccc cct ggt ggc gca gag tct gtg cac agc ttc tac Leu Ser Gly Ala Pro Pro Gly Gly Ala Glu Ser Val His Ser Phe Tyr 545 550 555	2043
cat gcc gac tgc cac tta gag cca gtc cgc tgc cag gag ccc cct ccc His Ala Asp Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro 560 565 570	2091
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gca cta gta gag gtg gct gcc agc tct ggg ccc cca acc ctc acc agc Ala Leu Val Glu Val Ala Ala Ser Ser Gly Pro Pro Thr Leu Thr Ser 610 615 620	2235
ctc aac atc cca ccc ggg ccc tac agc tcc atg cac aag ctg ctg gag Leu Asn Ile Pro Pro Gly Pro Tyr Ser Ser Met His Lys Leu Leu Glu 625 630 635	2283
aca cag agt aca ggt gcc tgc caa agc tct tgc aag atc tcc agc cct Thr Gln Ser Thr Gly Ala Cys Gln Ser Ser Cys Lys Ile Ser Ser Pro 640 645 650	2331
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16
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Asp Thr Phe Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile
735 740 745
atg atc gcc atc ctg gtc aac aca ctc agc atg ggc atc gaa tac cac 2667
Met Ile Ala Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His
750 755 760 765
gag cag ccc gag gag ctt acc aac gcc cta gaa atc agc aac atc gtc 2715
Glu Gln Pro Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val
770 775 780
ttc acc agc ctc ttt gcc ctg gag atg ctg ctg aag ctg ctt gtg tat 2763
Phe Thr Ser Phe Phe Ala Leu Glu Met Leu Leu Lys Leu Val Tyr
785 790 795
ggc ccc ttt ggc tac atc aag aat ccc tac aac atc ttc gat ggt gtc 2811
Gly Pro Phe Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val
800 805 810
att gtg gtc atc agc gtg tgg gag atc gtg ggc cag cag ggg ggc ggc 2859
Ile Val Val Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Gly
815 820 825
ctg tgg gtg ctg cgg acc ttc cgc ctg atg cgt gtg ctg aag ctg gtg 2907
Leu Ser Val Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val
830 835 840 845
cgc ttc ctg cgg gcc ctg cag cgg cag ctg gtg gtg ctc atg aag acc 2955
Arg Phe Leu Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr
850 855 860
atg gac aac gtg gcc acc ttc tgc atg ctg ctt atg ctc ttc atc ttc 3003
Met Asp Asn Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe
865 870 875
atc ttc agc atc ctg ggc atg cat ctc ttc gcc tgc aag ttt gcc tct 3051
Ile Phe Ser Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser
880 885 890
gag cgg gat ggg gac acc ctg cca gac cgg aag aat ttt gac tcc ttg 3099
Glu Arg Asp Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu
895 900 905
ctc tgg gcc atc gtc act gtc ttt cag atc ctg acc cag gag gac tgg 3147
Leu Trp Ala Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp
910 915 920 925
aac aaa gtc ctc tac aat ggt atg gcc tcc acg tgg tcc tgg ggc gcc 3195
Asn Lys Val Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala
930 935 940
ctt tat ttc att gcc ctc atg acc ttc ggc aac tac gtg ctc ttc aat 3243
Leu Tyr Phe Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn
945 950 955
ttg ctg gtc gcc att ctg gtg gag ggc ttc cag gcg gag gga gat gcc 3291
Leu Leu Val Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala
960 965 970

17

aac aag tcc gaa tca gag ccc gat ttc ttc tca ccc agc ctg gat ggt Asn Lys Ser Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Leu Asp Gly 975 980 985	3339
gat ggg gac agg aag aag tgc ttg gcc ttg gtg tcc ctg gga gag cac Asp Gly Asp Arg Lys Lys Cys Leu Ala Leu Val Ser Leu Gly Glu His 990 995 1000 1005	3387
ccg gag ctg cgg aag agc ctg ctg ccg cct ctc atc atc cac acg gcc Pro Glu Leu Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala 1010 1015 1020	3435
gcc aca ccc atg tgg ctg ccc aag agc acc agc acg ggc ctg ggc gag Ala Thr Pro Met Ser Leu Pro Lys Ser Thr Ser Thr Gly Leu Gly Glu 1025 1030 1035	3483
ggg ctg ggc cct ggc tgg cgc cgc acc agc agc agc ggg tgg gca gag Ala Leu Gly Pro Ala Ser Arg Arg Thr Ser Ser Ser Ser Ala Glu 1040 1045 1050	3531
cct ggg ggc gcc cac gag atg aag tca ccg ccc agc gcc cgc agc tct Pro Gly Ala Ala His Glu Met Lys Ser Pro Pro Ser Ala Arg Ser Ser 1055 1060 1065	3579
ccg cac agc ccc tgg agc gct gca agc agc tgg acc agc agg cgc tcc Pro His Ser Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser 1070 1075 1080 1085	3627
agc cgg aac agc ctc ggc cgt gca ccc agc ctg aag cgg aga agc cca Ser Arg Asn Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro 1090 1095 1100	3675
agt gga gag cgg cgg tcc ctg ttg tgg gga gaa ggc cag gag agc cag Ser Gly Glu Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln 1105 1110 1115	3723
gat gaa gag gag agc tca gaa gag gag cgg gcc agc cct ggc ggc agt Asp Glu Glu Glu Ser Ser Glu Glu Glu Arg Ala Ser Pro Ala Gly Ser 1120 1125 1130	3771
gac cat cgc cac agg ggg tcc ctg gag cgg gag gcc aag agt tcc ttt Asp His Arg His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe 1135 1140 1145	3819
gac ctg cca gac aca ctg cag gtg cca ggg ctg cat cgc act gcc agt Asp Leu Pro Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser 1150 1155 1160 1165	3867
ggc cga ggg tct gct tct gag cac cag gac tgc aat ggc aag tgg gct Gly Arg Gly Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala 1170 1175 1180	3915
tca ggg cgc ctg gcc cgg gcc ctg cgg cct gat gac ccc cca ctg gat Ser Gly Arg Leu Ala Arg Ala Leu Arg Pro Asp Asp Pro Pro Leu Asp 1185 1190 1195	3963
ggg gat gac gcc gat gac gag ggc aac ctg Gly Asp Asp Ala Asp Asp Glu Gly Asn Leu 1200 1205	3993

18

<210> 52
<211> 1207
<212> PRT
<213> Artificial Sequence

<220>
<223> CACNA1G - a gene encoding a T-type calcium channel

<400> 52
Met Asp Glu Glu Glu Asp Gly Ala Gly Ala Glu Glu Ser Gly Gln Pro
1 5 10 15
Arg Ser Phe Met Arg Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Pro
20 25 30
Gly Pro Gly Ser Ala Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
35 40 45
Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
50 55 60
Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
65 70 75 80
Pro Trp Phe Glu Arg Ile Ser Met Leu Val Ile Leu Leu Asp Cys Val
85 90 95
Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
100 105 110
Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe
115 120 125
Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile Phe Gly Lys
130 135 140
Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val
145 150 155 160
Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe
165 170 175
Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn
180 185 190
Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp Thr Leu
195 200 205
Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile
210 215 220
Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg
225 230 235 240
Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu
245 250 255
Arg Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser
260 265 270
Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu
275 280 285
Arg Gly Asp Gly Gly Gly Gly Pro Pro Cys Gly Leu Asp Tyr Glu Ala
290 295 300
Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr
305 310 315 320
Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly Ala Ile Asn
325 330 335
Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Thr
340 345 350
Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp Ala His Ser
355 360 365
Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser Phe
370 375 380
Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu
385 390 395 400

19

Thr	Lys	Gln	Arg	Glu	Ser	Gln	Leu	Met	Arg	Glu	Gln	Arg	Val	Arg	Phe
				405					410					415	
Leu	Ser	Asn	Ala	Ser	Thr	Leu	Ala	Ser	Phe	Ser	Glu	Pro	Gly	Ser	Cys
			420					425					430		
Tyr	Glu	Glu	Leu	Leu	Lys	Tyr	Leu	Val	Tyr	Ile	Leu	Arg	Lys	Ala	Ala
		435					440					445			
Arg	Arg	Leu	Ala	Gln	Val	Ser	Arg	Ala	Ala	Gly	Val	Arg	Val	Gly	Leu
	450					455				460					
Leu	Ser	Ser	Pro	Ala	Pro	Leu	Gly	Gly	Gln	Glu	Thr	Gln	Pro	Ser	Ser
465					470					475				480	
Ser	Cys	Ser	Arg	Ser	His	Arg	Arg	Leu	Ser	Val	His	His	Leu	Val	His
				485				490						495	
His	His	His	His	His	His	His	His	Tyr	His	Leu	Gly	Asn	Gly	Thr	Leu
			500					505					510		
Arg	Ala	Pro	Arg	Ala	Ser	Pro	Glu	Ile	Gln	Asp	Arg	Asp	Ala	Asn	Gly
	515						520				525				
Ser	Arg	Arg	Leu	Met	Leu	Pro	Pro	Pro	Ser	Thr	Pro	Ala	Leu	Ser	Gly
	530					535					540				
Ala	Pro	Pro	Gly	Gly	Ala	Glu	Ser	Val	His	Ser	Phe	Tyr	His	Ala	Asp
545					550					555				560	
Cys	His	Leu	Glu	Pro	Val	Arg	Cys	Gln	Ala	Pro	Pro	Pro	Arg	Ser	Pro
				565				570						575	
Ser	Glu	Ala	Ser	Gly	Arg	Thr	Val	Gly	Ser	Gly	Lys	Val	Tyr	Pro	Thr
			580					585					590		
Val	His	Thr	Ser	Pro	Pro	Pro	Glu	Thr	Leu	Lys	Glu	Lys	Ala	Leu	Val
	595						600					605			
Glu	Val	Ala	Ala	Ser	Ser	Gly	Pro	Pro	Thr	Leu	Thr	Ser	Leu	Asn	Ile
	610					615					620				
Pro	Pro	Gly	Pro	Tyr	Ser	Ser	Met	His	Lys	Leu	Leu	Glu	Thr	Gln	Ser
625					630					635				640	
Thr	Gly	Ala	Cys	Gln	Ser	Ser	Cys	Lys	Ile	Ser	Ser	Pro	Cys	Leu	Lys
				645				650						655	
Ala	Asp	Ser	Gly	Ala	Cys	Gly	Pro	Asp	Ser	Cys	Pro	Tyr	Cys	Ala	Arg
			660					665					670		
Ala	Gly	Ala	Gly	Glu	Val	Glu	Leu	Ala	Asp	Arg	Glu	Met	Pro	Asp	Ser
	675						680					685			
Asp	Ser	Glu	Ala	Val	Tyr	Glu	Phe	Thr	Gln	Asp	Ala	Gln	His	Ser	Asp
	690					695				700					
Leu	Arg	Asp	Pro	His	Ser	Arg	Arg	Gln	Arg	Ser	Leu	Gly	Pro	Asp	Ala
705					710					715				720	
Glu	Pro	Ser	Ser	Val	Leu	Ala	Phe	Trp	Arg	Leu	Ile	Cys	Asp	Thr	Phe
				725				730						735	
Arg	Lys	Ile	Val	Asp	Ser	Lys	Tyr	Phe	Gly	Arg	Gly	Ile	Met	Ile	Ala
			740					745					750		
Ile	Leu	Val	Asn	Thr	Leu	Ser	Met	Gly	Ile	Glu	Tyr	His	Glu	Gln	Pro
	755						760						765		
Glu	Glu	Leu	Thr	Asn	Ala	Leu	Glu	Ile	Ser	Asn	Ile	Val	Phe	Thr	Ser
	770					775					780				
Leu	Phe	Ala	Leu	Glu	Met	Leu	Leu	Lys	Leu	Leu	Val	Tyr	Gly	Pro	Phe
785					790					795				800	
Gly	Tyr	Ile	Lys	Asn	Pro	Tyr	Asn	Ile	Phe	Asp	Gly	Val	Ile	Val	Val
			805					810						815	
Ile	Ser	Val	Trp	Glu	Ile	Val	Gly	Gln	Gln	Gly	Gly	Gly	Leu	Ser	Val
			820				825						830		
Leu	Arg	Thr	Phe	Arg	Leu	Met	Arg	Val	Leu	Lys	Leu	Val	Arg	Phe	Leu
	835						840						845		
Pro	Ala	Leu	Gln	Arg	Gln	Leu	Val	Val	Leu	Met	Lys	Thr	Met	Asp	Asn
	850					855					860				
Val	Ala	Thr	Phe	Cys	Met	Leu	Leu	Met	Leu	Phe	Ile	Phe	Ile	Phe	Ser
865					870					875				880	

20

Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg Asp
 885 890 895
 Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp Ala
 900 905 910
 Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Lys Val
 915 920 925
 Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu Tyr Phe
 930 935 940
 Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu Val
 945 950 955 960
 Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Asn Lys Ser
 965 970 975
 Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Leu Asp Gly Asp Gly Asp
 980 985 990
 Arg Lys Lys Cys Leu Ala Leu Val Ser Leu Gly Glu His Pro Glu Leu
 995 1000 1005
 Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala Ala Thr Pro
 1010 1015 1020
 Met Ser Leu Pro Lys Ser Thr Ser Thr Gly Leu Gly Glu Ala Leu Gly
 1025 1030 1035 1040
 Pro Ala Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu Pro Gly Ala
 1045 1050 1055
 Ala His Glu Met Lys Ser Pro Pro Ser Ala Arg Ser Ser Pro His Ser
 1060 1065 1070
 Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser Ser Arg Asn
 1075 1080 1085
 Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro Ser Gly Glu
 1090 1095 1100
 Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln Asp Glu Glu
 1105 1110 1115 1120
 Glu Ser Ser Glu Glu Glu Arg Ala Ser Pro Ala Gly Ser Asp His Arg
 1125 1130 1135
 His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp Leu Pro
 1140 1145 1150
 Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly Arg Gly
 1155 1160 1165
 Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala Ser Gly Arg
 1170 1175 1180
 Leu Ala Arg Ala Leu Arg Pro Asp Asp Pro Pro Leu Asp Gly Asp Asp
 1185 1190 1195 1200
 Ala Asp Asp Glu Gly Asn Leu
 1205

<210> 53
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer for PCR (GAPDH)

<400> 53
 cggagtcac ggattggtcg tat

23

<210> 54
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

21

<223> primer for PCR (GAPDH)

<400> 54

agccttctcc atggtggtga agac

24

<210> 55

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Target sequence for bisulfite-PCR primer

<400> 55

aaaaaaccca aactacaaaa ac

22

<210> 56

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Target sequence for bisulfite-PCR primer

<221> misc_feature

<222> (0)...(0)

<223> r = G or A

<400> 56

gttggtgggrg ttggtggr

18

<210> 57

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Target sequence for bisulfite-PCR primer

<221> misc_feature

<222> (0)...(0)

<223> y = C or T

<400> 57

aactatcycc aacyccacaa

20

<210> 58

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Target sequence for bisulfite-PCR primer

<221> misc_feature

<222> (0)...(0)

<223> r = G or A

<400> 58

aagagatttt tttttttttt ttttgg

26

22

<210> 59
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<221> misc_feature
<222> (0)...(0)
<223> y = C or T

<400> 59
aaaatccyaa aaaaaacycc ccc

23

<210> 60
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<221> misc_feature
<222> (0)...(0)
<223> r = G or A

<400> 60
ggaagtttta ggggrgtagg ggaa

24

<210> 61
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<221> misc_feature
<222> (0)...(0)
<223> y = C or T

<400> 61
aacyatccct ccctctaacc tac

23

<210> 62
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<400> 62
aggtagtatg gtgaggtttg tttt

24

<210> 63
<211> 22
<212> DNA

23

<213> Artificial Sequence

<220>

<223> Target sequence for bisulfite-PCR primer

<221> misc_feature

<222> (0)...(0)

<223> r = G or A

<400> 63

atcaatacta aacraaatca aa

22

<210> 64

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Target sequence for bisulfite-PCR primer

<400> 64

aggaaaagaa aggtaaggg

19

<210> 65

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Target sequence for bisulfite-PCR primer

<221> misc_feature

<222> (0)...(0)

<223> r = G or A

<400> 65

caaaattaac rcaataaaaa aa

22

<210> 66

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Target sequence for bisulfite-PCR primer

<400> 66

tatttgaaga ggtggggaaa

20

<210> 67

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Target sequence for bisulfite-PCR primer

<400> 67

aaactcttac cccacctaac c

21

24

<210> 68
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<221> misc_feature
<222> (0)...(0)
<223> y = C or T

<400> 68
ggcttgtaat tggattaaay gtt

23

<210> 69
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<400> 69
ccactaactc aaaactaaaa aa

22

<210> 70
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<400> 70
gggagggtgta aaaggatgaa a

21

<210> 71
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<400> 71
ctaactactaa aataaaaata aa

22

<210> 72
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<221> misc_feature
<222> (0)...(0)
<223> y = C or T

25

<400> 72
gtaggatggt ataygaagag

20

<210> 73
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<221> misc_feature
<222> (0)...(0)
<223> r = G or A

<400> 73
aaacrctaac raacatacta c

21

<210> 74
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<400> 74
gggttttttt tagggtatatt

20

<210> 75
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<221> misc_feature
<222> (0)...(0)
<223> r = G or A

<400> 75
gaattaaatt tcaaaaaaac cr

22

<210> 76
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<221> misc_feature
<222> (0)...(0)
<223> y = C or T

<400> 76
tttaggagga tgyggagtt

19

<210> 77

26

<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<221> misc_feature
<222> (0)...(0)
<223> r = G or A

<400> 77
aaaaaaccta acraaacact ta

22

<210> 78
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<400> 78
gttattgtgt agtggagttt gg

22

<210> 79
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<221> misc_feature
<222> (0)...(0)
<223> r = G or A

<400> 79
actccrathta acaaaccaac

20

<210> 80
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<221> misc_feature
<222> (0)...(0)
<223> y = C or T

<400> 80
aatatgggtt yggttggtta

20

<210> 81
<211> 19
<212> DNA
<213> Artificial Sequence

27

<220>
<223> Target sequence for bisulfite-PCR primer

<400> 81
tccctaaatt ccacacatt

19

<210> 82
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<400> 82
gtaagttgta gttggttgg tta

23

<210> 83
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<221> misc_feature
<222> (0)...(0)
<223> r = G or A

<400> 83
ctctetacta ccraattcct ct

22

<210> 84
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<400> 84
gttttggttt tgggtgtg

18

<210> 85
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence for bisulfite-PCR primer

<400> 85
ccactaccaa acaaattcccc

20

<210> 86
<211> 19
<212> DNA
<213> Artificial Sequence

<220>

28

<223> Target sequence for bisulfite-PCR primer

<400> 86

tttattgggg aatttcggg

19

<210> 87

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Target sequence

<221> misc_feature

<222> (0)...(0)

<223> r = G or A

<400> 87

aacaaaataa ctactacrc ctc

23

<210> 88

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Target sequence

<400> 88

gtaaagtga ggggtggtgat g

21

<210> 89

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Target sequence

<221> misc_feature

<222> (0)...(0)

<223> r = G or A

<400> 89

ctccaaaaaa ctataaatac ccraa

25

<210> 90

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Target sequence

<221> misc_feature

<222> (0)...(0)

<223> y = C or T

<400> 90

gagtgaagtga aggyggtaga tt

22

29

<210> 91
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence

<221> misc_feature
<222> (0)...(0)
<223> r = G or A

<400> 91
aacctcacat taacrtctct aaa

23

<210> 92
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence

<400> 92
gttttttttaa gatbggggtt ttttag

26

<210> 93
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence

<400> 93
caaaccoccaa acatccttta toca

24

<210> 94
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence

<400> 94
ggatttaggg gtaaggggag gg

22

<210> 95
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence

<221> misc_feature
<222> (0)...(0)
<223> r = G or A

30

<400> 95
aaaaaccaca actaaaatcc ratt 24

<210> 96
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence

<400> 96
agtgagggat ttagttgtgg tgtg 24

<210> 97
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence

<221> misc_feature
<222> (0)...(0)
<223> r = G or A

<400> 97
aactatcacc aacrcacaa 20

<210> 98
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence

<221> misc_feature
<222> (0)...(0)
<223> y = C or T

<400> 98
aagagatttt tttttttttt ttttgt 26

<210> 99
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence

<221> misc_feature
<222> (0)...(0)
<223> r = G or A

<400> 99
aaaatccraa aaaaaacccc ccc 23

31

<210> 100
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence

<221> misc_feature
<222> (0)...(0)
<223> y = C or T

<400> 100
ggaagtttta ggggygtagg ggaa

24

<210> 101
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence

<400> 101
aacaaaatac aactcccaaa cacc

25

<210> 102
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence

<400> 102
ttagggtttg attttttaat ttggtt

26

<210> 103
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence

<221> misc_feature
<222> (0)...(0)
<223> r = G or A

<400> 103
caaaaaatta cratccccc tc

22

<210> 104
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Target sequence

32

<221> misc_feature

<222> (0)...(0)

<223> Y = C or T

<400> 104

ttggaggtat aataaggaga tttygg

26

<210> 105

<211> 576

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (0)...(0)

<223> APOB CpG ISLAND

<400> 105

ccggggaggc	gccctttgga	cctttttgaa	tcctggcgct	cttgcagcct	gggcttccta	60
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tcctcggttc	tgccgctgag	gagcccgccc	agccagccag	ggccgcgagg	ccgaggccag	180
gcccgcagcc	aggagccgcc	ccaccgcagc	tgccgatgga	cccgcggagg	cccgcgctgc	240
tggcgctgcc	tgcgctgctg	ctgctgctgc	tgccggggcg	caggggccgt	gagtgcggcg	300
ccgctctgcg	ggcagcagag	ggagcgggag	ggagcccgcg	gaccgaggtt	ggccggggca	360
gcctggggct	aggccagagg	gagggcagcc	acagggctca	gggcgagtgg	ggggattgga	420
ccagctggcg	gcccctgcag	gotcaggatg	ggggggcgcg	gatggagggg	ctgaggaggg	480
gggtctcggg	gcctgcctcc	ctcctgaaag	gtgaaacctg	tgccgggtgg	ccccctgtcg	540
ggccctctag	accgcctggg	aagacgtggg	aagctc			576

<210> 106

<211> 2093

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (0)...(0)

<223> CACNA1G CpG ISLAND

<400> 106

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ttggctccag	ccttcggggg	cggaccaggg	ggcaaggggg	ggggagaggg	gcggtcctgg	180
gtttttgggt	gggaatcgga	ttccagctgt	ggttctctcc	ctgcgctccc	gcccgcactg	240
ccacggcgga	ggccaatgg	gcgcgcggct	cggggcgggc	ggcgtccggc	gattggctgc	300
ggggctgtct	gggggcgggg	ccgaggcttg	aagttagaag	gagggatcca	gctgtgggtg	360
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gctgtggcgc	cggcgacagc	tacggcagcg	gcagccaccg	cggcggtctg	ggcggcggca	480
tctccgcctc	cactcccgcc	cgggaactgc	cccactgttc	tcccgcgcgc	tcccggacag	540
tgagcccgcg	gcggggcggg	ggaaggagcc	gccccacccc	cctccaagcc	cacccctaaa	600
gagatccctc	ctcccctccc	ccgcgcgctg	gcgcggagcc	gggacgatgc	tgacccctta	660
gatccgggtc	cagctgcgcc	gcgggaagag	ggggcgcccc	tcccgggacc	ccgcgcctcc	720
gocgctgccc	cccttttctg	tcgccccttc	ggggcggttc	cgccgaaggt	agcgcggaat	780
ccgggaaccc	gagcctgggg	gcgaagcgaa	gaagccggaa	caaagttagg	gggagccggc	840
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ctggccctcc	cgggggctca	gcttgcgccc	tagagccccc	cagatgtgcc	cccgcggggg	1020
cccccggttt	gcgctgaggac	acctcctctg	aggggcgcgc	cttgcccttc	tccggatcgc	1080
ccggggcccc	ggctggccag	aggatggacg	aggagggagg	tggagcgggc	gcccaggagt	1140
cgggacagcc	ccggagcttc	atgcggtcca	acgacctgtc	gggggcgggg	ggcggccggg	1200

33

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gccgggggtca gcagaaaagg acccggggcag cgcgggactcc gaggcggagg ggtgcccgtg 1260
ccgggcgctg gcccgggtgg ttttcttcta cttgagccag gacagccgcc cgcggagctg 1320
gtgtctccgc acggtctgta acccatatcc ttccggggcac gacggccagg cgcgggggtca 1380
gaaggggggac gggccgcacc gccgggggtc ggggggggag aagaccacac gccagggtgag 1440
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ccagagtggg agcggagacy cggagcaggtc tcttcggtaa cccgggctta cccacacctg 1560
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cctgcggggg tggaggcaca acaaggagat tccggcgggg gctgatgtca gggggcgaga 1980
atgagaacaa gatgtggtgg aggggagctg tctgccccg gagctgggag tggagccct 2040
ttccgctaga gccagtgcc gggggtgct cctaccgat ctccattcga tgc 2093

```

<210> 107

<211> 327

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (0)...(0)

<223> CDX2 CpG Island

<400> 107

```

ctcgttaatc acggaagccg ccggcctggg gctccgcacg ccagcctgtg cgggtctccc 60
ccgcctctgc agcctagtgg gaaggagggt ggaggaaaga aggaagaaag ggaggagggg 120
aggaggcagg ccaggaggag ggacccctc ggaggcagaa gagccgcagg gagccagcgg 180
agcaccgcgg gctggggcgc agccacccgc cgtccctcga gtccctcgc cctttccct 240
tcgtgcccc cggcagcctc cagcgtcggg cccagggcag catggtgagg tctgctccc 300
gtccctcgcc accatgtacg tgaagta 327

```

<210> 108

<211> 1663

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (0)...(0)

<223> EGFR CpG Island

<400> 108

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gtccgcgggg accgggtcca gaggggcagt gctgggaaag cccctctcgg aaattaaact 60
ctcaggggcac cgtccccctc ccatgggccg cccacctccc gccggagact aggtcccgcg 120
ggggccaccg tgtccaccgc ctccggggcg ctggccttgg gtcccgcgtg ctggttctcc 180
tccctcctcc tgcattcttc ctccctctct gctcctcccg atccctctcc cgcgcgctgg 240
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gcccgcggcg cagcgcggcc gcagcagcct cctccccccg cagcgtgtga gcgccgcgg 360
cgccgaggcg gccggagtcc cgaagtagcc ccgcggcccg cgcgcgccag accggacgac 420
aggccacctc gtccggtccc ccgagtcctc cgcctcgccg ccaacgccac aaccaccgag 480
cacggccccc tgaactccgtc cagtattgat cgggagagcc ggagcagact cttcggggag 540
cagcgtatgc accctccggg acggccgggg cagcgtctct ggogctgctg gctgcgctct 600
gcccggcgag tggggtctg gaggaaaaga aaggttaagg cgtgtctcgc ggctccccgc 660
cgcccccgga tgcgcgcccg gaccccgag cccgcaccaac cgcacgcgc accggcttcc 720
ccgcgcctcc cgcgcgtctt tctctgttct cttgagatca cgtgcgcgc cgaccgggac 780
cgccggaggg accgggacgtt tcttctctcg gccgggagag tctggggcg ggaggaggag 840
agacgcgtgg gacacgggac tgcaggccag gcggggaaag gccgcgggga cctccggcgc 900

```

34

cccgaaacggc	tcccaacttt	cttccctcac	tttcccccggc	cagctggcgca	ggatcggcgt	960
cagtggggcga	aagcgggggtg	ctgggtggggc	cctggggggcg	gggtcccgcga	ggggtctccc	1020
ggcgtgtcttt	cccaggggcgc	gacgggggttc	tggcgcgccac	ccgaggggcgg	ctgcccaccc	1080
ggcggagactg	cctgttttagg	gaagctgagg	aaggaaaccca	aaaatacagc	ctcggctcgg	1140
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cagggtgggggt	ccgaacccgcc	ccttggggcgc	agaccccggc	cgtcgcctc	gcccgggtg	1440
cctcgtcttt	gcctatccaa	gagtgccccc	cactccgggg	accccgagctc	cctccggcgc	1500
cggcgccgaaa	gccccagggtc	ctccttcgat	ggcgcctcgg	cggagacgtc	cgggtctcgt	1560
ccacctgcag	cccttcgggtc	gggcctggggc	ttcggcggtg	agcgggacgc	gggtgtccgg	1620
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<210> 109

<211> 1787

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (0)...(0)

<223> FBN1 CpG Island

<221> misc_feature

<222> (1)...(1787)

<223> n = A,T,C or G

<400> 109

agagcccgct	ctggagtggtg	ctctcgacac	ccaggggcaag	tggggggcggc	agagccctct	60
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tcccggcctc	cggcgtctgc	tgagtgctcg	gcggggagagg	cgcaggggagc	gcgtacccgg	180
gaggcggcgg	cagcgggggac	tgggtttctc	tccgggccaag	gcctccgggg	caaccgtctc	240
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ccacctcttc	ccatttctcc	cctcccacgc	tcaagacaaa	aagtcccagg	ccggggcagg	420
cctgacaccc	tctgcctcct	cccactgcgc	taattctgct	agcgagaggc	ccgcacccga	480
ggcggaggtc	gcaaaaggga	gtggaaaggg	aggatggatg	ggggcgggggg	gtgggggtgg	540
gatgagggcg	acgaaggagg	gggtgtcatt	ttctttttct	ttcttttttt	aaaaaaagta	600
ttctctctgc	gagaaaaccgc	tgcgcggagc	atacttgaag	aggtggggaa	aggagggggc	660
tgcgggagac	gcggcagaga	ctgtgggtgc	cacaagcgga	caggagccac	agctgggaca	720
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agcgggaccc	cggcgggcgc	gtgcgcttca	gggcgcagcg	gcggcgagcg	accgagcccc	1560
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gctggagatc	gcccctgggat	ttaccgtgct	tttagcgctc	tacacgagcc	atggggcgga	1680
cgccaaatttg	ggggctggga	acgtgaaagg	aaccagagcc	agtcggggcca	agaggaaggg	1740
cgggtggagga	cacgacgcgc	ttaaagggtg	aagggaacgg	ttccctc		1787

35

<210> 110
 <211> 810
 <212> DNA
 <213> Homo sapiens

<220>
 <221> gene
 <222> (0)...(0)
 <223> GPR37 CpG Island

<400> 110
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 cccctgttcc ctccagctc ctccgagtgg aagccgctac aaatggcttg aatgaaacgt 180
 gtgtgggttt agtgagtggg gaaccaaccag gggatcccggt cccccacaa accagtatct 240
 ctccgaggag gaggcgaagg agtgggagga ggcaacgagc cgagagtoga gcttcggcgg 300
 cgcgcgcagc ggctggagcg cgggggagag gccggggccac ctccccttcc cggcgcgcga 360
 ctgectggcc cgcggcggtt ccaggcacca ccttcccggt ccgggctgag cccgctgtgg 420
 cagtgactag ctcccgcggc tagcggcact gtccaccgac gagcgcgccc ctcttctccc 480
 ccttctccc accgatttct tctctgcggc ggcaacgctt ccagcagcct gcttcgcccc 540
 gtctcaact ttgagctgga ggagaagcaa ctttggcagt ggcgcggggg ttggaatccc 600
 gcttctctcc ggcagcagta ggctcgcaag tcgctggggg taggtggggc aagagtttcg 660
 ccggcgcatc agcgtgctt cggactgttt gcaacgtgtt tccagcgagc tgggagcggg 720
 gttgtgactg caggtcgtct gggggagggg gacttgtttt tcttttctc tagagacctc 780
 ggcttgcaac tggatcaaac gctgtcgaaa 810

<210> 111
 <211> 550
 <212> DNA
 <213> Homo sapiens

<220>
 <221> gene
 <222> (0)...(0)
 <223> HSPA6 CpG Island

<400> 111
 tgtattcgca tggtaacata tcttcgggtct tcttgcgctt gggctctcag cggccctcca 60
 aggcagcccg caggcccggtg ctgcgctcag ggatcctcca cagcncgggg gagaccttgc 120
 ctctaaagtt gctgcttttg cagctctgac acaaccgcgc gtccctcagag ccagccggga 180
 ggagctagaa ccttccccgc gtttctttca gcagccctga gtcagaggcg ggtggcctt 240
 gcaagttagc gccagcctt cttcggtctc acggaacgat ccgcccgaac cttctcccg 300
 ggtcagcgcc gcgctgcgcc gcccggtga ctcagcccg ggcggcgggc gggaggctct 360
 cgaactggcg ggaagggtgc ggaagggttc cggcgcgggg gtcggggagg tgcaaaagga 420
 tgaaaagccc gtggacggag ctgagcagat ccggccgggg tggcggcaga gaaacgcgag 480
 ggagagcctc actgctgagc gccctctgac ggcggcgggc gcagcctcag tggcctccag 540
 catccgacaa 550

<210> 112
 <211> 278
 <212> DNA
 <213> Homo sapiens

<220>
 <221> gene
 <222> (0)...(0)
 <223> IQGAP2 CpG Island

<400> 112
 agagttcact tttaactcag tctcagcgcg cggcgcccggt ggctggctct ggcgagagag 60

36

caaccgagga	gtgggtcgca	gatotttggg	gggttagggg	aaatggcgga	gaggcgggat	120
ccgagcgccg	cggcgggggg	cagagcccg	gagcctggcc	agcgagggtg	gcccgggggg	180
gcgcgccccg	ggcggggccc	cggagacggc	caggatgcca	caagaagagc	tgccgtcgct	240
gcagagaccc	cgctatgggt	ctattgtgga	cgatgaaa			278

<210> 113
<211> 1461
<212> DNA
<213> Homo sapiens

<220>
<221> gene
<222> (0)...(0)
<223> KL CpG Island

<400> 113						
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ccttttcagc	cacggcggaag	ttccccctcg	gctgtcccoac	ctggcagtc	ctotaggatt	120
tcggccagtc	cctaattggc	tccagcaatg	tccagccgga	gcttotttgg	gctcccgagt	180
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ccgcgccccg	agtggggaaa	agttgttcgg	cgcttttctt	ccccgacgaa	gcccgtccag	300
gggtgctctc	agaggacggc	cggcaggcaa	agagaatgaa	cctgagcgtc	cacgaaacgt	360
cctgcacggc	tcccgggagc	tgggagaaa	aggtgccttt	ctccgacgtc	cgcggggcgac	420
gcctgcgcga	ccttgcccg	tgccgcggcc	ctcccgggga	ccctcgccc	tcggcgcccc	480
tgccccccac	cccagtgcca	gggcgggagg	agtcocggct	cgcaggtaat	tattgcoagc	540
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cagcgccccc	cgcgcggccc	cgcggcgccc	gcgcgcgctg	ctgtcgctgc	tgctgggtgt	720
gctgggctcg	ggcgcccgcc	gcctgcgtgc	ggagccgggc	gaogcgcgcg	agacctgggc	780
ccgtttctcg	cggcctcctg	cccccgaggc	cgcgggcttc	ttccagggca	ccttccccga	840
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ctccgggaac	gccagctctg	cgttgggcgc	cccgctgcgc	ctgcagcccg	ccaccggggg	1020
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cgtccccaac	cgcgaggggg	tgcgctacta	cggcgcgctg	ctggagcggc	tgccggagct	1200
ggggcgctgc	cccgctggta	cctgtatcca	ctgggacgtg	cccgagcgcc	tgagggacgc	1260
ctacggcgcc	tggggccaac	gcgcctctgg	cgaaccactt	agggattacg	cggagctctg	1320
cttcggccac	ttggcggtgc	aggtcaagta	ctggatcacc	atcgacaacc	cctacgtggt	1380
ggcctggcac	ggctacgcca	ccggggcgct	ggcccccggc	atccggggca	gcccgcgggt	1440
cgggtacctg	gtggcgccaca	a				1461

<210> 114
<211> 249
<212> DNA
<213> Homo sapiens

<220>
<221> gene
<222> (0)...(0)
<223> PAR2 CpG Island

<400> 114						
ccccgggctt	ggcctcccg	aggtgagtac	gctgctcctt	cggtttccct	gaaacctaac	60
ccgcctctgg	gagggcgcca	gcagaggctc	cgattcgggg	caggtgagag	gctgacttct	120
ttctcggtgc	tccagtgagg	ctctgagttt	cgaatcgccg	gcggcgagat	ccccgcgcgc	180
cggcgctcgg	ggcttccagg	aggatgcgga	gccccagcgc	ggcgtgggtg	ctggggggcg	240
ccatcctgc						249

<210> 115

37

<211> 709
 <212> DNA
 <213> Homo sapiens

<220>
 <221> gene
 <222> (0)...(0)
 <223> PITX2 CpG Island

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<400> 115
agtcggtggt cctgctcctc gggtgggtcc taagtgcgcc gccaggtccc ctctcctttc      60
gctctcccggt ctcgggtccc cgaactctcg gccggtggc atctggttcc ctccctgccc      120
tcgtttctctg tcgcccctgc tcgctccccc cggcggtcgc ccgggcgctg tgcctgctcc      180
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tttggtggaa tctctgctga cgtcacgtca ctcccacac ggagtaggag cagagggaag      300
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gcttgccgtg cagccggagg ctccgctcgc tggaaatcgc ccgggaagc agtgggacgc      540
ggagacagca gctctctccc ggtagccgat aacggggaaa tggagacca ctgccgcaa      600
ctgggtgtcgg cgtgtctgca attagagaaa gataaaagcc agcaggggaa gaatgaggac      660
gtgggcgcgc aggaccgctc taagaagaag cggcaaaagg ggcagcggg      709
  
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<210> 116
 <211> 1496
 <212> DNA
 <213> Homo sapiens

<220>
 <221> gene
 <222> (0)...(0)
 <223> PTCA CpG Island

<221> misc_feature
 <222> (1)...(1496)
 <223> n = A,T,C or G

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<400> 116
ggggccgcag cggcagcagc gcccgcggtg tgagcagcag cagcggtcgg tctgtcaacc      60
ggagcccgag cccgagcagc ctgcggccag cagcgtctcc gcaagccgag cggccaggcg      120
cgccaggagc ccgcagcagc ggcagcagcg cgcggggcgc ccggggaagc ctccgtcccc      180
gcggcgggcg cggcgggggc ggcaacatgg cctcggtcgg taacgcgcgc gagcccgagg      240
accgcggcgg cggcgggcagc ggctgtatcg gtgcccgggg accgcgggct ggaggcggga      300
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ggcccagcta ctgcgacgcc gccttcgntn nggagnagat ttncanngn nggcatttca      420
gaatntntcn ttcccacttt ntcttccent acctntaact cntnggggat cggcccccgc      480
acacacaaac acacacactn tcttctctcn tntctcacac acaacacaca cactcaactca      540
caatctctca ggaagagcag cagacaaatg gggattgaaa aattcaaaac ctccctctgg      600
tnntgggagg aaagggctgt ctgaggtccg cagggggtgg aggtgtgtgt gtgtgcgtgt      660
gtgtgtgtgn anacacacgc ootccctggg gtgccttttc cggagcaact gaaagccgtc      720
cacggcgga caccctcaagg gggcgcgcgc ggtcgtagcg gtagtagcgt tcgctcgtgt      780
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gcgttttctg aagtcagagc ttttaggcgc ttaggagttc gtagtagcgg tagtagcgcg      900
tcgggtcgtt cgggaagtgt tcgttttcgc ggcggcgggc gggcgggcgg taatatgggt      960
tcgggttggt acgtcgtcga gttttaggat cgcggcgggc ggggtagcgg ttgtatcggt      1020
gtttcgggac ggtcgggttg agggcgggag cgtagacgga cggggggggt gcgtcgtgt      1080
gtcgcgtcgg atcgggatta tttgtatcgg ttttagttat gcgacgtcgt tttcgtntng      1140
gagnagattt nttangngng gtattttaga tttntntnt tttattttnt tttttntat      1200
ttntaatctn tnggggatcg ttttcgttat atataaatat atatatntt tttttntnt      1260
ttttatatat aatatatata tttatttata tntttntagg aaaagtagta gataaatggg      1320
  
```

38

```

gattgaaaaa tttaaatttt ttttttggtt ntgggaggaa aggggttgtt gaggttcgta 1380
gggggtggag gtgtgtgtgt gtgctgtgtgt gtgtgtgnan atatacgttt tttttgggtgt 1440
gttttttttcg gagtattgga aagtcgttta cggcgggatta ttttaagggc ggtcgt 1496

```

<210> 117

<211> 701

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (0)...(0)

<223> PTCHB CpG Island

<221> misc_feature

<222> (1)...(701)

<223> n = A,T,C or G

<400> 117

```

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tgcccttatt tgcagcctaa actcctgtac ggctgccaca tttcttaaca tcttggaggg 120
ggaggcggag tggagagagg cggagagagg aagggggggg ggagccgaaa taaagggtgt 180
ttcctttttt ggcagccagt tttgggtttt ttgagcatga aatctctgtt ccttataaaa 240
attattctcg gaaaaagata tccccccgtt ttccagggtt ttgagccgco tctccttagg 300
gcctgggtcg gggaggaaaa gttgttaaca aattgccacc ttaaattcgc ggtgcganc 360
tgccggagctg ccgggttcat tgtgtttacg aggtctcgtg aaatgtgtgg aatccaggga 420
aggcagagcac ccagacgggg gcccgccggg gcggcggcca gcgcggggga aatgccgcgc 480
cggggagcag catgcgcggg cctgagccct tccctttgca ctgggtgttt ttttacgttt 540
aaccagaaag gaagggagag gagggaaaaga tccatgtggc tgccctcttc cgatcacaaa 600
tattgtcgta agttgcagct ggctgcccga ntctctaatt cagctcacac agcntntccc 660
cacgctatgg aaatgcgtcg ggagtgaact ccggcggcgc c 701

```

<210> 118

<211> 273

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (0)...(0)

<223> SDC1 CpG Island

<400> 118

```

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cagccggcgg accctgcagc cctcgcctgg gacagcggcg cgttgggcag gcgcccaga 120
gagcatcgag cagcggaaac cgcgaagccg gcccgagcc gcgaccgcgc cagcctgccg 180
ctctcccgcc gccggtccgg gcagcatgag gcgcgcggcg ctctggctct gggtgtgcgc 240
gctggcgctg agcctgcagc tggccctgcc gca 273

```

<210> 119

<211> 751

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (0)...(0)

<223> SDC4 CpG Island

<400> 119

39

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gcgcagtgcc ccgcaggccct cgcctccact ggggaattcc gggcggggtg cggcgggcg 120
ggcggggggcg ggcggggggcg ggcggggtag gcgcctata agatgggtg cgcgcggcc 180
cggggccact cgcgcagcc tgcgcgctt ctccagtcg cggtgccatg gcccccgcc 240
gtctgttcgc gctgctgctg ttcttcgtag ggcgagtcg cagtcggtg ggtgcttga 300
ggttcccggg ctggggggcga agcgggggcg caggccggtg cctcctttgt tcgtcggagc 360
gtgggatggg gggggggcaga tcgggggtac gctacccca accggacacc gaggcccg 420
aaactttgtt ggaaactttt ctccggggtc acggggccag ctcgggatg gcttcacgc 480
ccgtgcgccc ctgcctgtt gcttttccc cctcccggg cctcagccc gcgcgggct 540
acgggctcgt tagtgactaa gccgggtgtc actcttcaac tcccacacc tcgtccctt 600
cctgggtgacc ctggggcagg cttggagcgc tgaatccct cctcgctctc gggggcgcca 660
gagcagacag ctttaggata cagatggcc ctgggggtcg gggggctgag tgtactcga 720
agggggaggg ttttaggggt gtgcgaggcc c 751
```

<210> 120

<211> 673

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA fragment termed MINT31

<221> misc_feature

<222> (1) ... (673)

<223> n = A,T,C or G

<400> 120

```
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aggggaagaag gtgtcagacg cggggagcaa ccataaatag ccccccttcc ccagaagacg 120
gcacgggggtt caagactcag gcgcgcata ctcaaatga gagcagagac tccgcgcagg 180
aaaaaaagggc acttagggga tctgctcatt aacatgaaat gcaaatgagc ccgcccggcc 240
tcattttacac aaactctgtc atggattcgg cgaaaaggga accagggaga cgaaggcgca 300
gcagccactc tgccacttcc cccatccct ccccccac cggcggggcg ggaactgaga 360
cgaccccaac cctctgcggc ggcgggaggt gcgcggggc tgctgggtg gtgcagcctt 420
aggggagtg acaacgccc ggggtgatg cctcagcaa gtgaggggtg gtgatggagg 480
tcattccgac catcccgcc cctctcggca gtggcgcaag cgcgcacaaa tctccggaga 540
nggaactgag tgaccacta ggttccgccc tgtctacct tcgcagatgt tggggaagt 600
cttcccgccg tctaatcctc gctgttccc cctccaccg cgcacagcac acccgggcg 660
ctccgctccc ggg 673
```